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#9
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1632

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/310,638

DATE: 05/16/2001

TIME: 15:13:30

Input Set : A:\MUL-P307.txt

Output Set: N:\CRF3\05162001\I310638.raw

SEQUENCE LISTING

ENTERED

(1) GENERAL INFORMATION:

(i) APPLICANT: Soreq, Hermona
Zakut, Haim
Shani, Moshe

(ii) TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
ANTICHOLINESTERASE SUBSTANCES

(iii) NUMBER OF SEQUENCES: 27

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Kohn & Associates
(B) STREET: 30500 Northwestern Hwy, Suite 410
(C) CITY: Farmington Hills
(D) STATE: Michigan
(E) COUNTRY: US
(F) ZIP: 48334

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/09/310,638
C--> 31 (B) FILING DATE: 12-May-1999
32 (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kohn, Kenneth I.
(B) REGISTRATION NUMBER: 30,955
(C) REFERENCE/DOCKET NUMBER: P-307 (Mulford)

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (810) 539-5050
(B) TELEFAX: (810) 539-5055

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

58	CCTCTCTCCC	CTCATCTTTG	CCAACCTGCC	CCACCTCCTC	TGCAGCTGAG	CGATAACCCT	60
60	TGGGCCGACA	GTGCCCTAAT	CTCCTCCCTC	CTGGCTTCTC	GACCGACCCT	TCACCCTTTC	120
62	CCTTTCTTTT	TCCAGCAGA	CGCCGCCTGC	CCTGCAGCCA	TGAGGCCCCC	GCAGTGTCTG	180
64	CTGCACACGC	CTTCCCTGGC	TTCCCCACTC	CTTCTCTCC	TCCTCTGGCT	CCTGGGTGGA	240
66	GGAGTGGGGG	CTGAGGGCCG	GGAGGATGCA	GAGCTGTCTG	TGACGGTGCG	TGGGGGCCGG	300
68	CTGCGGGGCA	TTGCCTGAA	GACCCCGGG	GGCCCTGTCT	CTGCTTTCCT	GGGCATCCCC	360
70	TTTGCGGAGC	CACCCATGGG	ACCCCGTCGC	TTTCTGCCAC	CGGAGCCCAA	GCAGCCTTGG	420
72	TCAGGGGTGG	TAGACGCTAC	AACCTTCCAG	AGTGTCTGCT	ACCAATATGT	GGACACCCTA	480
74	TACCCAGGTT	TTGAGGGCAC	CGAGATGTGG	AACCCCAACC	GTGAGCTGAG	CGAGGACTGC	540

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76 CTGTACCTCA ACGTGTGGAC ACCATACCCC CGGCCTACAT CCCCCACCCC TGTCTCGTC      600
78 TGGATCTATG GGGGTGGCTT CTACAGTGGG GCCTCCTCCT TGGACGTGTA CGATGGCCGC      660
80 TTCTTGGTAC AGGCCGAGAG GACTGTGCTG GTGTCCATGA ACTACCGGT GGGAGCCTTT      720
82 GGCTTCCTGG CCCTGCCGGG GAGCCGAGAG GCCCCGGGCA ATGTGGGTCT CCTGGATCAG      780
84 AGGCTGGCCC TTCACTGGGT GACGAGAACC GTGGCAGCCT TCGGGGGTGA CCCGACATCA      840
86 GTGACGCTGT TTGGGGAGAG CGCGGGAGCC GCCTCGGTGG GCATGCACCT GCTGTCCCCG      900
88 CCCAGCCGGG GCCTGTTCCT CAGGGCCGTG CTGCAGAGCG GTGCCCCCAA TGGACCCTGG      960
90 GCCACGGTGG GCATGGGAGA GGGCCGTCGC AGGGCCACGC AGCTGGCCCA CCTTGTGGGC      1020
92 TGTCTCCAG GCGGCACTGG TGGGAATGAC ACAGAGCTGG TAGCCTGCCT TCGGACACGA      1080
94 CCAGCGCAGG TCCTGGTGAA CCACGAATGG CACGTGCTGC CTCAAGAAAG CGTCTCCGG      1140
96 TTCTCCTTCG TGCCTGTGGT AGATGGAGAC TTCCTCAGTG ACACCCAGAG GGGCCTCATC      1200
98 AACGCGGGAG ACTTCACCGG CCTGCAGGTG CTGGTGGGTG TGGTGAAGGA TGAGGGCTCG      1260
100 TATTTTCTGG TTTACGGGGC CCCAGGCTTC AGCAAAGACA ACGAGTCTCT CATCAGCCGG      1320
102 GCCGAGTTCC TGGCCGGGGT GCGGGTCGGG GTTCCCCAGG TAAGTGACCT GGCAGCCGAG      1380
104 GCTGTGGTCC TGCATTACAC AGACTGGCTG CATCCCAGAG ACCCGGCACG CCTGAGGGAG      1440
106 GCCCTGAGCG ATGTGGTGGG CGACCACAAT GTCGTGTGCC CCGTGGCCCA GCTGGCTGGG      1500
108 CGACTGGCTG CCCAGGGTGC CCGGGTCTAC GCCTACGTCT TTGAACACCG TGCTTCCACG      1560
110 CTCTCCTGGC CCCTGTGGAT GGGGGTGCCC CACGGCTACG AGATCGAGTT CATCTTGGG      1620
112 ATCCCCCTGG ACCCTCTCG AAACCTACAG GCAGAGGAGA AAATCTTCGC CCAGCGACTG      1680
114 ATGCGATACT GGGCCAATT TGCCCGCACA GGGGATCCCA ATGAGCCCCG AGACCCCAAG      1740
116 GCCCCACAAT GGGCCCCGTA CACGGCGGGG GCTCAGCAGT ACGTTAGTCT GGACCTGCGG      1800
118 CCGCTGGAGG TGCGCGGGG GCTGCGCGCC CAGGCCTGCG CCTTCTGGAA CCGCTTCCTC      1860
120 CCAAATTCG TCAGCGCCAC CGACACGCTC GACGAGGCGG AGCGCCAGTG GAAGGCCGAG      1920
122 TTCCACCGCT GGAGCTCCTA CATGGTGCAC TGGAAGAACC AGTTCGACCA CTACAGCAAG      1980
124 CAGGATCGCT GCTCAGACCT GTGACCCCGG CGGGACCCCG ATGTCCCTCG CTCCGCCCG      2040
126 CCCCCTAGCT GTATATACTA TTTATTTTCA GGCTGGGCTA TAACACAGAC GAGCCCCAGA      2100
128 CTCTGCCCAT CCCCACCCCA CCCCACGTC CCCCAGGGCT CCCGGTCCTC TGGCATGTCT      2160
130 TCAGGCTGAG CTCTCCCCG CGTGCCTTCG CCCTCTGGCT GCAAATAAAC TGTTACAGGC      2220
132 CAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA      2256

```

134 (2) INFORMATION FOR SEQ ID NO: 2:

136 (i) SEQUENCE CHARACTERISTICS:

137 (A) LENGTH: 614 amino acids

138 (B) TYPE: amino acid

139 (C) STRANDEDNESS: single

140 (D) TOPOLOGY: linear

146 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

148 Met Arg Pro Pro Gln Cys Leu Leu His Thr Pro Ser Leu Ala Ser Pro
149 1 5 10 15
151 Leu Leu Leu Leu Leu Leu Trp Leu Leu Gly Gly Gly Val Gly Ala Glu
152 20 25 30
154 Gly Arg Glu Asp Ala Glu Leu Leu Val Thr Val Arg Gly Gly Arg Leu
155 35 40 45
157 Arg Gly Ile Arg Leu Lys Thr Pro Gly Gly Pro Val Ser Ala Phe Leu
158 50 55 60
160 Gly Ile Pro Phe Ala Glu Pro Pro Met Gly Pro Arg Arg Phe Leu Pro
161 65 70 75 80
163 Pro Glu Pro Lys Gln Pro Trp Ser Gly Val Val Asp Ala Thr Thr Phe
164 85 90 95
166 Gln Ser Val Cys Tyr Gln Tyr Val Asp Thr Leu Tyr Pro Gly Phe Glu

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167																	
169	Gly	Thr	Glu	Met	Trp	Asn	Pro	Asn	Arg	Glu	Leu	Ser	Glu	Asp	Cys	Leu	
170				115				120					125				
172	Tyr	Leu	Asn	Val	Trp	Thr	Pro	Tyr	Pro	Arg	Pro	Thr	Ser	Pro	Thr	Pro	
173		130					135					140					
175	Val	Leu	Val	Trp	Ile	Tyr	Gly	Gly	Gly	Phe	Tyr	Ser	Gly	Ala	Ser	Ser	
176	145					150					155					160	
178	Leu	Asp	Val	Tyr	Asp	Gly	Arg	Phe	Leu	Val	Gln	Ala	Glu	Arg	Thr	Val	
179					165						170					175	
181	Leu	Val	Ser	Met	Asn	Tyr	Arg	Val	Gly	Ala	Phe	Gly	Phe	Leu	Ala	Leu	
182				180					185						190		
184	Pro	Gly	Ser	Arg	Glu	Ala	Pro	Gly	Asn	Val	Gly	Leu	Leu	Asp	Gln	Arg	
185			195					200					205				
187	Leu	Ala	Leu	Gln	Trp	Val	Gln	Glu	Asn	Val	Ala	Ala	Phe	Gly	Gly	Asp	
188		210					215					220					
190	Pro	Thr	Ser	Val	Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	
191		225				230					235					240	
193	Gly	Met	His	Leu	Leu	Ser	Pro	Pro	Ser	Arg	Gly	Leu	Phe	His	Arg	Ala	
194					245					250						255	
196	Val	Leu	Gln	Ser	Gly	Ala	Pro	Asn	Gly	Pro	Trp	Ala	Thr	Val	Gly	Met	
197				260					265							270	
199	Gly	Glu	Ala	Arg	Arg	Arg	Ala	Thr	Gln	Leu	Ala	His	Leu	Val	Gly	Cys	
200			275					280					285				
202	Pro	Pro	Gly	Gly	Thr	Gly	Gly	Asn	Asp	Thr	Glu	Leu	Val	Ala	Cys	Leu	
203		290					295					300					
205	Arg	Thr	Arg	Pro	Ala	Gln	Val	Leu	Val	Asn	His	Glu	Trp	His	Val	Leu	
206		305				310					315					320	
208	Pro	Gln	Glu	Ser	Val	Phe	Arg	Phe	Ser	Phe	Val	Pro	Val	Val	Asp	Gly	
209				325						330					335		
211	Asp	Phe	Leu	Ser	Asp	Thr	Pro	Glu	Ala	Leu	Ile	Asn	Ala	Gly	Asp	Phe	
212				340					345					350			
214	His	Gly	Leu	Gln	Val	Leu	Val	Gly	Val	Val	Lys	Asp	Glu	Gly	Ser	Tyr	
215			355					360					365				
217	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	Phe	Ser	Lys	Asp	Asn	Glu	Ser	Leu	
218		370					375					380					
220	Ile	Ser	Arg	Ala	Glu	Phe	Leu	Ala	Gly	Val	Arg	Val	Gly	Val	Pro	Gln	
221		385				390					395					400	
223	Val	Ser	Asp	Leu	Ala	Ala	Glu	Ala	Val	Val	Leu	His	Tyr	Thr	Asp	Trp	
224				405						410							

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241   Thr Ala Glu Glu Lys Ile Phe Ala Gln Arg Leu Met Arg Tyr Trp Ala
242               500               505               510
244   Asn Phe Ala Arg Thr Gly Asp Pro Asn Glu Pro Arg Asp Pro Lys Ala
245               515               520               525
247   Pro Gln Trp Pro Pro Tyr Thr Ala Gly Ala Gln Gln Tyr Val Ser Leu
248               530               535               540
250   Asp Leu Arg Pro Leu Glu Val Arg Arg Gly Leu Arg Ala Gln Ala Cys
251               545               550               555               560
253   Ala Phe Trp Asn Arg Phe Leu Pro Lys Leu Leu Ser Ala Thr Asp Thr
254               565               570               575
256   Leu Asp Glu Ala Glu Arg Gln Trp Lys Ala Glu Phe His Arg Trp Ser
257               580               585               590
259   Ser Tyr Met Val His Trp Lys Asn Gln Phe Asp His Tyr Ser Lys Gln
260               595               600               605
262   Asp Arg Cys Ser Asp Leu
263               610
265 (2) INFORMATION FOR SEQ ID NO: 3:
267   (i) SEQUENCE CHARACTERISTICS:
268       (A) LENGTH: 3096 base pairs
269       (B) TYPE: nucleic acid
270       (C) STRANDEDNESS: single
271       (D) TOPOLOGY: linear
275   (ix) FEATURE:
276       (A) NAME/KEY: CDS
277       (B) LOCATION: 160..1959
280   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
282 CCTCTCTCCC CTCATCTTTG CCAACCTGCC CCACCTCTC TGCAGCTGAG CGATAACCCT      60
284 TGGGCCGACA GTGCCCTAAT CTCCTCCCTC CTGGCTTCTC GACCGACCCT TCACCCTTTC      120
286 CTTTCTTTC TCCCAGCAGA CGCCGCCTGC CCTGCAGCC ATG AGG CCC CCG CAG      174
287                               Met Arg Pro Pro Gln
288                               1               5
290 TGT CTG CTG CAC ACG CCT TCC CTG GCT TCC CCA CTC CTT CTC CTC CTC      222
291 Cys Leu Leu His Thr Pro Ser Leu Ala Ser Pro Leu Leu Leu Leu Leu
292               10               15               20
294 CTC TGG CTC CTG GGT GGA GGA GTG GGG GCT GAG GGC CGG GAG GAT GCA      270
295 Leu Trp Leu Leu Gly Gly Gly Val Gly Ala Glu Gly Arg Glu Asp Ala
296               25               30               35
298 GAG CTG CTG GTG ACG GTG CGT GGG GGC CGG CTG CGG GGC ATT CGC CTG      318
299 Glu Leu Leu Val Thr Val Arg Gly Gly Arg Leu Arg Gly Ile Arg Leu
300               40               45               50
302 AAG ACC CCC GGG GGC CCT GTC TCT GCT TTC CTG GGC ATC CCC TTT GCG      366
303 Lys Thr Pro Gly Gly Pro Val Ser Ala Phe Leu Gly Ile Pro Phe Ala
304               55               60               65
306 GAG CCA CCC ATG GGA CCC CGT CGC TTT CTG CCA CCG GAG CCC AAG CAG      414
307 Glu Pro Pro Met Gly Pro Arg Arg Phe Leu Pro Pro Glu Pro Lys Gln
308       70               75               80               85
310 CCT TGG TCA GGG GTG GTA GAC GCT ACA ACC TTC CAG AGT GTC TGC TAC      462
311 Pro Trp Ser Gly Val Val Asp Ala Thr Thr Phe Gln Ser Val Cys Tyr
312               90               95               100

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314	CAA	TAT	GTG	GAC	ACC	CTA	TAC	CCA	GGT	TTT	GAG	GGC	ACC	GAG	ATG	TGG	510
315	Gln	Tyr	Val	Asp	Thr	Leu	Tyr	Pro	Gly	Phe	Glu	Gly	Thr	Glu	Met	Trp	
316				105					110				115				
318	AAC	CCC	AAC	CGT	GAG	CTG	AGC	GAG	GAC	TGC	CTG	TAC	CTC	AAC	GTG	TGG	558
319	Asn	Pro	Asn	Arg	Glu	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	Trp	
320			120					125					130				
322	ACA	CCA	TAC	CCC	CGG	CCT	ACA	TCC	CCC	ACC	CCT	GTC	CTC	GTC	TGG	ATC	606
323	Thr	Pro	Tyr	Pro	Arg	Pro	Thr	Ser	Pro	Thr	Pro	Val	Leu	Val	Trp	Ile	
324		135					140						145				
326	TAT	GGG	GGT	GGC	TTC	TAC	AGT	GGG	GCC	TCC	TCC	TTG	GAC	GTG	TAC	GAT	654
327	Tyr	Gly	Gly	Gly	Phe	Tyr	Ser	Gly	Ala	Ser	Ser	Leu	Asp	Val	Tyr	Asp	
328	150				155					160					165		
330	GGC	CGC	TTC	TTG	GTA	CAG	GCC	GAG	AGG	ACT	GTG	CTG	GTG	TCC	ATG	AAC	702
331	Gly	Arg	Phe	Leu	Val	Gln	Ala	Glu	Arg	Thr	Val	Leu	Val	Ser	Met	Asn	
332				170					175					180			
334	TAC	CGG	GTG	GGA	GCC	TTT	GGC	TTC	CTG	GCC	CTG	CCG	GGG	AGC	CGA	GAG	750
335	Tyr	Arg	Val	Gly	Ala	Phe	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Ser	Arg	Glu	
336			185						190					195			
338	GCC	CCG	GGC	AAT	GTG	GGT	CTC	CTG	GAT	CAG	AGG	CTG	GCC	CTG	CAG	TGG	798
339	Ala	Pro	Gly	Asn	Val	Gly	Leu	Leu	Asp	Gln	Arg	Leu	Ala	Leu	Gln	Trp	
340			200					205						210			
342	GTG	CAG	GAG	AAC	GTG	GCA	GCC	TTC	GGG	GGT	GAC	CCG	ACA	TCA	GTG	ACG	846
343	Val	Gln	Glu	Asn	Val	Ala	Ala	Phe	Gly	Gly	Asp	Pro	Thr	Ser	Val	Thr	
344		215				220						225					
346	CTG	TTT	GGG	GAG	AGC	GCG	GGA	GCC	TCG	GTG	GGC	ATG	CAC	CTG	CTG		894
347	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ser	Val	Gly	Met	His	Leu	Leu		
348	230					235				240				245			
350	TCC	CCG	CCC	AGC	CGG	GGC	CTG	TTC	CAC	AGG	GCC	GTG	CTG	CAG	AGC	GGT	942
351	Ser	Pro	Pro	Ser	Arg	Gly	Leu	Phe	His	Arg	Ala	Val	Leu	Gln	Ser	Gly	
352				250					255					260			
354	GCC	CCC	AAT	GGA	CCC	TGG	GCC	ACG	GTG	GGC	ATG	GGA	GAG	GCC	CGT	CGC	990
355	Ala	Pro	Asn	Gly	Pro	Trp	Ala	Thr	Val	Gly	Met	Gly	Glu	Ala	Arg	Arg	
356			265						270					275			
358	AGG	GCC	ACG	CAG	CTG	GCC	CAC	CTT	GTG	GGC	TGT	CCT	CCA	GGC	GGC	ACT	1038
359	Arg	Ala	Thr	Gln	Leu	Ala	His	Leu	Val	Gly	Cys	Pro	Pro	Gly	Gly	Thr	
360			280					285						290			
362	GGT	GGG	AAT	GAC	ACA	GAG	CTG	GTA	GCC	TGC	CTT	CGG	ACA	CGA	CCA	GCG	1086
363	Gly	Gly	Asn	Asp	Thr	Glu	Leu	Val	Ala	Cys	Leu	Arg	Thr	Arg	Pro	Ala	
364		295				300						305					
366	CAG	GTC	CTG	GTG	AAC	CAC	GAA	TGG	CAC	GTG	CTG	CCT	CAA	GAA	AGC	GTC	1134
367	Gln	Val	Leu	Val	Asn	His	Glu	Trp	His	Val	Leu	Pro	Gln	Glu	Ser	Val	
368	310				315					320				325			
370	TTC	CGG	TTC	TCC	TTC	GTG	CCT	GTG	GTA	GAT	GGA	GAC	TTC	CTC	AGT	GAC	1182
371	Phe	Arg	Phe	Ser	Phe	Val	Pro	Val	Val	Asp	Gly	Asp	Phe	Leu	Ser	Asp	
372				330						335				340			
374	ACC	CCA	GAG	GCC	CTC	ATC	AAC	GCG	GGA	GAC	TTC	CAC	GGC	CTG	CAG	GTG	1230
375	Thr	Pro	Glu	Ala	Leu	Ile	Asn	Ala	Gly	Asp	Phe	His	Gly	Leu	Gln	Val	
376			345						350					355			
378	CTG	GTG	GGT	GTG	GTG	AAG	GAT	GAG	GGC	TCG	TAT	TTT	CTG	GTT	TAC	GGG	1278

VERIFICATION SUMMARY

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Input Set : A:\MUL-P307.txt

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L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:629 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:633 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:637 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:641 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:645 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:649 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:653 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:657 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:661 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:665 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:669 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:673 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:677 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:681 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:685 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:689 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:693 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:697 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:701 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:705 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:709 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:713 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:717 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:721 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:725 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:729 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:733 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:737 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:741 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:745 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:749 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:753 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:757 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:761 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:765 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:769 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:773 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:777 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
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L:785 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:1332 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:26
L:1336 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:26